

X12553.ST25.txt
SEQUENCE LISTING

<110> Eli Lilly and Company
<120> Erythropoietic Compounds
<130> X-12553
<140> US 09/856,451
<141> 2001-05-22
<150> PCT/US99/27801
<151> 1999-11-23
<160> 4
<170> PatentIn version 3.2
<210> 1
<211> 168
<212> PRT
<213> Artificial Sequence
<220>
<223> synthetic construct

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa at position 1 is absent or Met;

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa at position 2 is absent or is Ala, Cys, Asp, Glu, Phe, Gly, His, Ile, Leu, Met, Asn, Gln, Arg, Ser, Thr, Val, Trp, or Tyr

<220>
<221> MISC_FEATURE
<222> (26)..(26)
<223> Xaa at position 26 is Asn, Lys or Glu;

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Xaa at position 40 is Asn, Lys or Glu;

<220>
<221> MISC_FEATURE
<222> (78)..(78)
<223> Xaa at position 78 is Arg or Glu;

<220>
<221> MISC_FEATURE
<222> (85)..(85)
<223> Xaa at position 85 is Asn, Lys or Glu;

<220>
<221> MISC_FEATURE
<222> (90)..(90)
<223> Xaa at position 90 is Trp, Lys, Pro, or Arg;

<220>
<221> MISC_FEATURE
<222> (128)..(128)
<223> Xaa at position 128 is Ser, Thr, Lys or Glu;

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<220>
<221> MISC_FEATURE
<222> (141)..(141)
<223> Xaa at position 141 is Arg or Glu;

<220>
<221> MISC_FEATURE
<222> (156)..(156)
<223> Xaa at position 156 is Lys or Glu; and

<220>
<221> MISC_FEATURE
<222> (168)..(168)
<223> Xaa at position 168 is Arg, absent, or any other amino acid.

<400> 1

Xaa Xaa Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg
1 5 10 15

Tyr Leu Leu Glu Ala Lys Glu Ala Glu xaa Ile Thr Thr Gly Cys Ala
20 25 30

Glu His Cys Ser Leu Asn Glu xaa Ile Thr Val Pro Asp Thr Lys Val
35 40 45

Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu
50 55 60

Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Xaa Gly Gln
65 70 75 80

Ala Leu Leu Val Xaa Ser Ser Gln Pro Xaa Glu Pro Leu Gln Leu His
85 90 95

Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg
100 105 110

Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Xaa
115 120 125

Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Xaa Lys Leu Phe
130 135 140

Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Xaa Leu Tyr Thr Gly
145 150 155 160

Glu Ala Cys Arg Thr Gly Asp Xaa
165

<210> 2
<211> 193
<212> PRT
<213> homo sapiens

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<400> 2

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Ser Leu
1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
20 25 30

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
35 40 45

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
50 55 60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
65 70 75 80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
85 90 95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
100 105 110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
130 135 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
180 185 190

Arg

<210> 3
<211> 498
<212> DNA
<213> homo sapiens

<400> 3
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gttccggaca ccaaagttaa cttctacgct tggaaacgta tggaaagggtgg tcagcaggct 180
gttgaagttt ggcagggtct ggctctgctg tccgaagctg ttctgcgtgg tcaggctctg 240

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ctggtaact cctcccagcc gtggaaaccg ctgcagctgc acgttgacaa agctgttcc 300
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ccgccccgacg ctgcttccgc tgctccgctg cgtaccatca ccgctgacac cttccgtaaa 420
ctgttccgtg tttactccaa cttcctgcgt ggtaaactga aactgtacac cggtgaagct 480
tgccgtaccg gtgactga 498

<210> 4
<211> 165
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 4

Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu
1 5 10 15

Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His
20 25 30

Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
35 40 45

Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
50 55 60

Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
65 70 75 80

Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
85 90 95

Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
100 105 110

Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
115 120 125

Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
130 135 140

Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
145 150 155 160

Cys Arg Thr Gly Asp
165